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Virulence determinants within the E2 glycoprotein of Classical Swine Fever Virus

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Classical Swine Fever is a highly contagious disease of pigs caused by Classical Swine Fever Virus (CSFV), a member of the *pestivirus* genus within the family *Flaviviridae*. The E2 glycoprotein of CSFV has been shown to be an important factor for the virulence of the virus. In a recent study, we have identified a specific motif within the E2 glycoprotein that contributes to the virulence of the highly virulent CSFV strain Koslov (Fahnøe et al. 2014). This motif comprises residues S74 and L75 in the N-terminal domain of E2 (S763 and L764 in the polyprotein). Evidence points towards involvement of this motif in virulence. CSFV strains encoding L763 and P764 represent the predominant alleles across all published full-length CSFV genomes, whereas the S763/L764 combination is only seen in highly virulent strains. In this study, mutations were introduced into the consensus cDNA clone of the highly virulent CSFV strain Koslov to evaluate the virulence of a set of E2 mutants with modifications in the encoded residues 763 and 764; these mutants are termed; vKos_SP, vKos_LP and vKos_LL, respectively. Animal infection experiments were performed to compare virulence of these E2 mutants in comparison to vKos (with the SL motif). The results indicate that the E2 residues 763-64 play an important role in CSFV virulence.

References

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